

SEQUENCE LISTING

<110> YOKOYAMA, KEIICHI
NAKAMURA, NAMI
MIWA, TETSUYA
SEGURO, KATSUYA

<120> PROCESS FOR PRODUCING MICROBIAL TRANSGLUTAMINASE

<130> 0010-0937-0

<140> 09/109,063

<141> 1998-07-02

<150> JP 180010/1997

<151> 1997-07-04

<160> 62

<170> PatentIn Ver. 2.0

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Asn	Tyr	Ile	Arg	Lys	Trp	Gln	Gln	Val	Tyr	Ser	His	Arg	Asp	Gly	Arg
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Lys	Gln	Gln	Met	Thr	Glu	Glu	Gln	Arg	Glu	Trp	Leu	Ser	Tyr	Gly	Cys
	50					55				60					
Val	Gly	Val	Thr	Trp	Val	Asn	Ser	Gly	Gln	Tyr	Pro	Thr	Asn	Arg	Leu
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Ala	Phe	Ala	Ser	Phe	Asp	Glu	Asp	Arg	Phe	Lys	Asn	Glu	Leu	Lys	Asn
				85					90					95	
Gly	Arg	Pro	Arg	Ser	Gly	Glu	Thr	Arg	Ala	Glu	Phe	Glu	Gly	Arg	Val
			100					105					110		
Ala	Lys	Glu	Ser	Phe	Asp	Glu	Glu	Lys	Gly	Phe	Gln	Arg	Ala	Arg	Glu
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Val	Ala	Ser	Val	Met	Asn	Arg	Ala	Leu	Glu	Asn	Ala	His	Asp	Glu	Ser
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Ala	Tyr	Leu	Asp	Asn	Leu	Lys	Lys	Glu	Leu	Ala	Asn	Gly	Asn	Asp	Ala
45					150					155					160
Leu	Arg	Asn	Glu	Asp	Ala	Arg	Ser	Pro	Phe	Tyr	Ser	Ala	Leu	Arg	Asn
				165					170					175	
Thr	Pro	Ser	Phe	Lys	Glu	Arg	Asn	Gly	Gly	Asn	His	Asp	Pro	Ser	Arg
			180					185					190		
Met	Lys	Ala	Val	Ile	Tyr	Ser	Lys	His	Phe	Trp	Ser	Gly	Gln	Asp	Arg
		195					200					205			
Ser	Ser	Ser	Ala	Asp	Lys	Arg	Lys	Tyr	Gly	Asp	Pro	Asp	Ala	Phe	Arg
	210					215					220				
Pro	Ala	Pro	Gly	Thr	Gly	Leu	Val	Asp	Met	Ser	Arg	Asp	Arg	Asn	Ile
225					230					235					240
Pro	Arg	Ser	Pro	Thr	Ser	Pro	Gly	Glu	Gly	Phe	Val	Asn	Phe	Asp	Tyr
				245					250					255	
Gly	Trp	Phe	Gly	Ala	Gln	Thr	Glu	Ala	Asp	Ala	Asp	Lys	Thr	Val	Trp
			260					265					270		
Thr	His	Gly	Asn	His	Tyr	His	Ala	Pro	Asn	Gly	Ser	Leu	Gly	Ala	Met
		275					280					285			
His	Val	Tyr	Glu	Ser	Lys	Phe	Arg	Asn	Trp	Ser	Glu	Gly	Tyr	Ser	Asp
	290					295					300				
Phe	Asp	Arg	Gly	Ala	Tyr	Val	Ile	Thr	Phe	Ile	Pro	Lys	Ser	Trp	Asn
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48

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cca gat cca tat cgt cca tct tat ggt cgt gct gaa act gtt gtt aat 96 Pro Asp Pro Tyr Arg Pro Ser Tyr Gly Arg Ala Glu Thr Val Val Asn	20				25				30							
aat tat att cgt aaa tgg caa caa gtt tat tct cat cgt gat ggt cgt 144 Asn Tyr Ile Arg Lys Trp Gln Gln Val Tyr Ser His Arg Asp Gly Arg	35				40				45							
aaa caa caa atg act gaa gaa caa cgt gaa tgg ctg tct tat ggt tgc 192 Lys Gln Gln Met Thr Glu Glu Gln Arg Glu Trp Leu Ser Tyr Gly Cys	50				55				60							
gtt ggt gtt act tgg gtt aac tct ggt cag tat ccg act aac cgt ctg 240 Val Gly Val Thr Trp Val Asn Ser Gly Gln Tyr Pro Thr Asn Arg Leu	65				70				75				80			
gca ttc gct tcc ttc gat gaa gat cgt ttc aag aac gaa ctg aag aac 288 Ala Phe Ala Ser Phe Asp Glu Asp Arg Phe Lys Asn Glu Leu Lys Asn	85				90				95							
ggg cgt ccg cgt tct ggt gaa act cgt gct gaa ttc gaa ggt cgt gtt 336 Gly Arg Pro Arg Ser Gly Glu Thr Arg Ala Glu Phe Glu Gly Arg Val	100				105				110							
gct aag gaa tcc ttc gat gaa gag aaa ggc ttc cag cgt gct cgt gaa 384 Ala Lys Glu Ser Phe Asp Glu Glu Lys Gly Phe Gln Arg Ala Arg Glu	115				120				125							
gtt gct tct gtt atg aac cgt gct cta gag aac gct cat gat gaa tct 432 Val Ala Ser Val Met Asn Arg Ala Leu Glu Asn Ala His Asp Glu Ser	130				135				140							
gct tac ctg gat aac ctg aag aag gaa ctg gct aac ggt aac gat gct 480 Ala Tyr Leu Asp Asn Leu Lys Lys Glu Leu Ala Asn Gly Asn Asp Ala	145				150				155				160			
ctg cgt aac gaa gat gct cgt tct ccg ttc tac tct gct ctg cgt aac 528 Leu Arg Asn Glu Asp Ala Arg Ser Pro Phe Tyr Ser Ala Leu Arg Asn	165				170				175							
act ccg tcc ttc aaa gaa cgt aac ggt ggt aac cat gat ccg tct cgt 576 Thr Pro Ser Phe Lys Glu Arg Asn Gly Gly Asn His Asp Pro Ser Arg	180				185				190							
atg aaa gct gtt atc tac tct aaa cat ttc tgg tct ggt cag gat aga 624 Met Lys Ala Val Ile Tyr Ser Lys His Phe Trp Ser Gly Gln Asp Arg	195				200				205							
tct tct tct gct gat aaa cgt aaa tac ggt gat ccg gat gca ttc cgt 672 Ser Ser Ser Ala Asp Lys Arg Lys Tyr Gly Asp Pro Asp Ala Phe Arg	210				215				220							
ccg gct ccg ggt act ggt ctg gta gac atg tct cgt gat cgt aac atc 720 Pro Ala Pro Gly Thr Gly Leu Val Asp Met Ser Arg Asp Arg Asn Ile																

225	230					235					240					
ccg cgt tct ccg act tct ccg ggt gaa ggc ttc gtt aac ttc gat tac	Pro Arg Ser Pro Thr	245	Pro Gly Glu Gly Phe Val Asn Phe Asp Tyr	255	768											
ggg tgg ttc ggt gct cag act gaa gct gat gct gat aag act gta tgg	Gly Trp Phe Gly Ala Gln Thr Glu Ala Asp Ala Asp Lys Thr Val Trp	260	265	270	816											
acc cat ggt aac cat tac cat gct ccg aac ggt tct ctg ggt gct atg	Thr His Gly Asn His Tyr His Ala Pro Asn Gly Ser Leu Gly Ala Met	275	280	285	864											
cat gta tac gaa tct aaa ttc cgt aac tgg tct gaa ggt tac tct gac	His Val Tyr Glu Ser Lys Phe Arg Asn Trp Ser Glu Gly Tyr Ser Asp	290	295	300	912											
ctc gat cgt ggt gct tac gtt atc acc ttc att ccg aaa tct tgg aac	Phe Asp Arg Gly Ala Tyr Val Ile Thr Phe Ile Pro Lys Ser Trp Asn	305	310	315	320	960										
act gct ccg gac aaa gtt aaa cag ggt tgg ccg	Thr Ala Pro Asp Lys Val Lys Gln Gly Trp Pro	325	330		993											
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Met Asp Ser Asp Asp Arg Val Thr Pro																
1 5																
 cca gct gaa cca ctg gat cgt atg cca gat cca tat cgt cca tct tat 161																
Pro Ala Glu Pro Leu Asp Arg Met Pro Asp Pro Tyr Arg Pro Ser Tyr																
10 15 20 25																
 ggg cgt gct gaa act gtt gtt aat aat tat att cgt aaa tgg caa caa 209																
Gly Arg Ala Glu Thr Val Val Asn Asn Tyr Ile Arg Lys Trp Gln Gln																
30 35 40																
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Val Tyr Ser His Arg Asp Gly Arg Lys Gln Gln Met Thr Glu Glu Gln																

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cgt	gaa	tgg	ctg	tct	tat	ggt	tgc	ggt	ggt	ggt	act	tgg	ggt	aac	tct	305		
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Gly	Gln	Tyr	Pro	Thr	Asn	Arg	Leu	Ala	Phe	Ala	Ser	Phe	Asp	Glu	Asp			
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cgt	ttc	aag	aac	gaa	ctg	aag	aac	ggt	cgt	ccg	cgt	tct	ggt	gaa	act	401		
Arg	Phe	Lys	Asn	Glu	Leu	Lys	Asn	Gly	Arg	Pro	Arg	Ser	Gly	Glu	Thr			
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cgt	gct	gaa	ttc	gaa	ggt	cgt	ggt	gct	aag	gaa	tcc	ttc	gat	gaa	gag	449		
Arg	Ala	Glu	Phe	Glu	Gly	Arg	Val	Ala	Lys	Glu	Ser	Phe	Asp	Glu	Glu			
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aaa	ggc	ttc	cag	cgt	gct	cgt	gaa	ggt	gct	tct	ggt	atg	aac	cgt	gct	497		
Lys	Gly	Phe	Gln	Arg	Ala	Arg	Glu	Val	Ala	Ser	Val	Met	Asn	Arg	Ala			
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cta	gag	aac	gct	cat	gat	gaa	tct	gct	tac	ctg	gat	aac	ctg	aag	aag	545		
Leu	Glu	Asn	Ala	His	Asp	Glu	Ser	Ala	Tyr	Leu	Asp	Asn	Leu	Lys	Lys			
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gaa	ctg	gct	aac	ggt	aac	gat	gct	ctg	cgt	aac	gaa	gat	gct	cgt	tct	593		
Glu	Leu	Ala	Asn	Gly	Asn	Asp	Ala	Leu	Arg	Asn	Glu	Asp	Ala	Arg	Ser			
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ccg	ttc	tac	tct	gct	ctg	cgt	aac	act	ccg	tcc	ttc	aaa	gaa	cgt	aac	641		
Pro	Phe	Tyr	Ser	Ala	Leu	Arg	Asn	Thr	Pro	Ser	Phe	Lys	Glu	Arg	Asn			
	170				175					180					185			
ggt	ggt	aac	cat	gat	ccg	tct	cgt	atg	aaa	gct	ggt	atc	tac	tct	aaa	689		
Gly	Gly	Asn	His	Asp	Pro	Ser	Arg	Met	Lys	Ala	Val	Ile	Tyr	Ser	Lys			
				190					195					200				
cat	ttc	tgg	tct	ggt	cag	gat	aga	tct	tct	tct	gct	gat	aaa	cgt	aaa	737		
His	Phe	Trp	Ser	Gly	Gln	Asp	Arg	Ser	Ser	Ser	Ala	Asp	Lys	Arg	Lys			
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Tyr	Gly	Asp	Pro	Asp	Ala	Phe	Arg	Pro	Ala	Pro	Gly	Thr	Gly	Leu	Val			
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gac	atg	tct	cgt	gat	cgt	aac	atc	ccg	cgt	tct	ccg	act	tct	ccg	ggt	833		
Asp	Met	Ser	Arg	Asp	Arg	Asn	Ile	Pro	Arg	Ser	Pro	Thr	Ser	Pro	Gly			
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gaa	ggc	ttc	ggt	aac	ttc	gat	tac	ggt	tgg	ttc	ggt	gct	cag	act	gaa	881		
Glu	Gly	Phe	Val	Asn	Phe	Asp	Tyr	Gly	Trp	Phe	Gly	Ala	Gln	Thr	Glu			
	250				255					260					265			
gct	gat	gct	gat	aag	act	gta	tgg	acc	cat	ggt	aac	cat	tac	cat	gct	929		
Ala	Asp	Ala	Asp	Lys	Thr	Val	Trp	Thr	His	Gly	Asn	His	Tyr	His	Ala			

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ccg aac ggt tct ctg ggt gct atg cat gta tac gaa tct aaa ttc cgt			977
Pro Asn Gly Ser Leu Gly Ala Met His Val Tyr Glu Ser Lys Phe Arg			
285	290	295	
aac tgg tct gaa ggt tac tct gac ttc gat cgt ggt gct tac gtt atc			1025
Asn Trp Ser Glu Gly Tyr Ser Asp Phe Asp Arg Gly Ala Tyr Val Ile			
300	305	310	
acc ttc att ccg aaa tct tgg aac act gct ccg gac aaa gtt aaa cag			1073
Thr Phe Ile Pro Lys Ser Trp Asn Thr Ala Pro Asp Lys Val Lys Gln			
315	320	325	
ggt tgg ccg taatgaaagc ttggatctct aattactgga cttcacacag			1122
Gly Trp Pro			
330			
actaaaatag acatatctta tattatgtga ttttgtgaca tttcctagat gtgaggtgga			1182
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gcgcacagg tgcggttgct ggcgccctata tcgccgacat caccgatggg gaagatcggg			1302
ctcgccactt cgggctcatg agcgcttggt tcggcgtggg tatggtggca ggccccgtgg			1362
ccgggggact gttggggcgcc atctccttgc atgcaccatt ccttgccggcg gcggtgctca			1422
acggectcaa cctactactg ggctgcttcc taatgcagga gtcgcataag ggagagcgtc			1482
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 <213> Artificial Sequence

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<210> 6
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 <210> 9
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 <210> 10
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<210> 13
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<210> 15
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 <210> 16
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 <212> DNA
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 <210> 17
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211> 35
 212> DNA
 213> Artificial Sequence

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 223> Description of Artificial Sequence:SYNTHETIC DNA

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 210> 21
 211> 35
 212> DNA
 213> Artificial Sequence

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 223> Description of Artificial Sequence:SYNTHETIC DNA

 400> 21
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 210> 22
 211> 48
 212> DNA
 213> Artificial Sequence

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 223> Description of Artificial Sequence:SYNTHETIC DNA

 400> 22
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 210> 23
 211> 48
 212> DNA
 213> Artificial Sequence

 220>
 223> Description of Artificial Sequence:SYNTHETIC DNA

 400> 23
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 210> 24
 211> 42
 212> DNA
 213> Artificial Sequence

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 223> Description of Artificial Sequence:SYNTHETIC DNA

 400> 24

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<210> 26
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
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<210> 27
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<210> 28
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<210> 29
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 223> Description of Artificial Sequence:SYNTHETIC DNA
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 210> 30
 211> 40
 212> DNA
 213> Artificial Sequence
 220>
 223> Description of Artificial Sequence:SYNTHETIC DNA
 400> 30
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 210> 31
 211> 39
 212> DNA
 213> Artificial Sequence
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 210> 32
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 212> DNA
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 400> 33
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 210> 34

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 <223> Description of Artificial Sequence:SYNTHETIC DNA

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 <210> 38
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210> 39

211> 48

212> DNA

213> Artificial Sequence

220>

223> Description of Artificial Sequence:SYNTHETIC DNA

400> 39

atcacgaga catgtctacc agaccagtac ccggagccgg acggaatg

48

210> 40

211> 35

212> DNA

213> Artificial Sequence

220>

223> Description of Artificial Sequence:SYNTHETIC DNA

400> 40

tgatcgtaa catcccgcgt tctccgactt ctccg

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210> 41

211> 36

212> DNA

213> Artificial Sequence

220>

223> Description of Artificial Sequence:SYNTHETIC DNA

400> 41

ttcacccgg agaagtcgga gaacgcggga tggttac

36

210> 42

211> 40

212> DNA

213> Artificial Sequence

220>

223> Description of Artificial Sequence:SYNTHETIC DNA

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210> 43

211> 40

212> DNA

213> Artificial Sequence

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 <400> 43
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 <223> Description of Artificial Sequence:SYNTHETIC DNA
 <400> 44
 ctgagactga agctgatgct gataagactg tatggaccga tgga 44
 <210> 45
 <211> 41
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Description of Artificial Sequence:SYNTHETIC DNA
 <400> 45
 agcttccatg ggtccatata gtcttatcag catcagcttc a 41
 <210> 46
 <211> 39
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Description of Artificial Sequence:SYNTHETIC DNA
 <400> 46
 aattcccatg gtaaccatta ccatgctccg aacggttct 39
 <210> 47
 <211> 42
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Description of Artificial Sequence:SYNTHETIC DNA
 <400> 47
 caccagaga accgttcgga gcatggtaat ggttaccatg gg 42
 <210> 48

<211> 41
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence:SYNTHETIC DNA

 <400> 48
 ctgggtgcta tgcattgtata cgaatctaaa ttccgtaact g 41

 <210> 49
 <211> 42
 <212> DNA
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 <220>
 <223> Description of Artificial Sequence:SYNTHETIC DNA

 <400> 49
 cttcagacca gttacggaat ttagattcgt atacatgcat ag 42

 <210> 50
 <211> 37
 <212> DNA
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 <220>
 <223> Description of Artificial Sequence:SYNTHETIC DNA

 <400> 50
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 <210> 51
 <211> 37
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence:SYNTHETIC DNA

 <400> 51
 gtgataacgt aagcaccacg atcgaagtca gagtaac 37

 <210> 52
 <211> 38
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence:SYNTHETIC DNA

 <400> 52

ttatcacct tcattccgaa atcttggaac actgctcc

38

<210> 53

<211> 38

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:SYNTHETIC DNA

<400> 53

ctttgtccgg agcagtgttc caagatttcg gaatgaag

38

<210> 54

<211> 38

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:SYNTHETIC DNA

<400> 54

ggacaaagtt aaacagggtt ggccgtaatg aaagctta

38

<210> 55

<211> 34

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:SYNTHETIC DNA

<400> 55

agcttaagct ttcattacgg ccaaccctgt ttaa

34

<210> 56

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:SYNTHETIC DNA

<400> 56

ttttcccagt cacgacgttg

20

<210> 57

<211> 21

<212> DNA

<213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:SYNTHETIC DNA
 <400> 57
 caggaaacag ctatgaccat g 21
 <210> 58
 <211> 36
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Description of Artificial Sequence:SYNTHETIC DNA
 <400> 58
 taaggagggt taaaatgtct gacgatcgtg ttactc 36
 <210> 59
 <211> 21
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Description of Artificial Sequence:SYNTHETIC DNA
 <400> 59
 tacgccaagg ttgttaaccc a 21
 <210> 60
 <211> 5
 <212> PRT
 <213> Artificial Sequence
 <220>
 <223> Description of Artificial Sequence:N-TERMINAL
 FRAGMENT
 <400> 60
 Ser Asp Asp Arg Val
 1 5
 <210> 61
 <211> 15
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Description of Artificial Sequence:CODON FOR
 N-TERMINAL FRAGMENT
 <400> 61
 tctgacgatc gtgtt 15

<210> 62
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:N-TERMINAL
FRAGMENT

<400> 62
Met Ser Asp Asp Arg
1 5

Met Ser Asp Asp Arg
1 5